

INTERNATIONAL CITRUS GENOMICS CONSORTIUM.
VALENCIA DECLARATION
9 April 2003

We, the undersigned, as delegates of the initial Citrus Genomics Consortium Meeting, consider:

That citrus is the main fruit tree crop in the world. In addition to its agronomical and economical importance, the citrus industry has great social and cultural interest as part of our heritage. Its potential interest as a model system for studying biological and biotechnological traits of general application to other tree crops should also be considered.

Problems and Limitations of Citrus Breeding

Traditional breeding as a genetic improvement strategy for citrus cultivar development faces many serious impediments. There are biological limitations associated with degrees of sexual sterility and incompatibility, that prevent the utilization of certain breeding parents and exploitation of specific parental combinations. There is widespread nucellar embryony (asexual seed production) within many of the commercially significant species, that limits opportunities for recombination and segregation of desirable alleles. For most citrus species, extended juvenility imposes the serious constraint of multi-year generation cycle length and decreases the speed with which genetic progress can be realized. Large individual plant size and consequent expenses of land, labor, and materials required to maintain and to grow progeny to maturity limit the number of crosses and the size of segregating families that can be produced. The consequence of these limitations is reduced probability of acquiring and identifying superior individual offspring that represent the most desirable combination of alleles for the traits that should be improved. Finally, and perhaps more significantly, the most economically important citrus cultivar groups (sweet oranges, grapefruit, most lemons, Satsumas and Clementines) likely originated from unique individual seedlings. All subsequent diversification within these groups has been through the process of identification of spontaneously occurring somatic mutations. Two consequences follow from these facts. First, there is minimal genetic and allelic diversity within these cultivar groups which constrains and restricts opportunity for genetic advance. Second, it is extremely difficult if not impossible to create new and improved cultivars that will produce fruit which consumers recognize as typical and possessing characteristics associated with sweet orange, grapefruit, lemon, or Clementine and satsuma mandarin. To retain these essential characteristics and to achieve significant improvements in critical traits demands the application of genetic improvement techniques other than traditional breeding through sexual hybridization and selection. Although some of these obstacles can be reduced by currently available methods such as marker-assisted selection, somatic hybridization and mutation breeding, such methods are currently useful for only a few traits and populations because the citrus genome is poorly characterized.

The Promise of Genomic Technology

Genomic technology can provide all citrus researchers with a new set of tools to address the problems and limitations described above. Genomics includes methods to rapidly identify and manipulate genes that influence desirable and undesirable traits. When the biological mechanisms responsible for these characters are understood, citrus breeders can develop improved varieties more rapidly and predictably than is currently possible. Genomics also should provide tools that allow growers to optimize production practices

and use more environmentally friendly pest and disease control strategies. Development of new varieties using genomic tools also will benefit consumers by providing fruit with enhanced flavor, quality, nutritional and biofunctional (health) value. Recently, the understanding of many aspects of plant biology has increased very rapidly because of collaborative research to sequence the genomes of a model dicot plant, *Arabidopsis thaliana* and a monocot crop plant, rice. The information from these projects is often difficult to apply to citrus for two reasons. First, these species are distantly related to citrus, and second, citrus is a perennial tree crop whose economic product is a fruit developmentally very different from those of *Arabidopsis* and rice. Citrus genome analysis will build on the foundation established by other plant genome projects, providing unique information applicable not only to citrus but also to other woody perennials. Overall, a citrus genome project will develop tools that make variety improvement, production, and post harvest management more efficient and predictable. These changes will benefit growers, consumers, and society.

Benefits of an International Collaborative Project

The magnitude of the effort required for an integrated genomics project is too large for a single citrus research institute to fund and undertake. Therefore, we have agreed to organize an International Citrus Genomics Consortium which objective is the development of a set of genomic tools for use in citrus research worldwide. The organization will foster research cooperation, organization, and sharing to leverage resources, enabling achievement of objectives that exceed the capacity of individual institutes. Information generated by the Consortium will be shared among its members for use in their research. The Consortium has selected sweet orange (*Citrus sinensis*) as the model for study because of its scientific and commercial importance.

In this constituent act, we designated Vicente Conejero, as president of the Steering Committee for 2003-2004, with the compromise of coordinating the elaboration of a White Paper, in about three months, that reflects the nature and general objectives, as well as, the work plan for the specific objectives, and serves as the means through which our common ventures will be presented to the institutions managing the science and technology in our countries.

Specific Objectives of the Consortium

The specific objectives agreed upon by the Consortium members are generation of:

- an EST database
- a consensus linkage map
- a physical map
- functional genomic tools
- development of a fast cycling transformation system
- bioinformatic tools
- whole genome sequence

We believe that these tools will greatly expand our knowledge of citrus genetics and biology, and thereby facilitate development of improved citrus cultivars and production practices. Thus, at this initial meeting, the undersigned researchers from Australia, Brazil, China, France, Israel, Italy, Japan, Spain, and the USA agree to collaborate and coordinate efforts to develop and share these tools and projects. Membership in the Consortium is open to others willing to be active participants in achieving our objectives.

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VALENCIA, SPAIN 7-11 APRIL 2003

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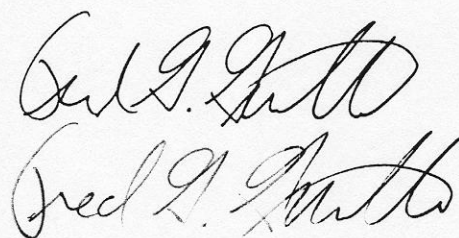
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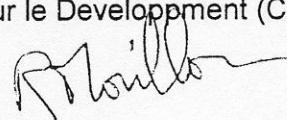
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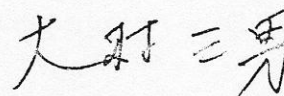
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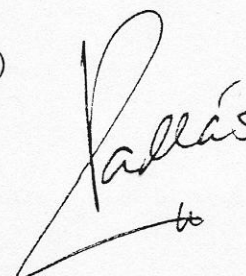
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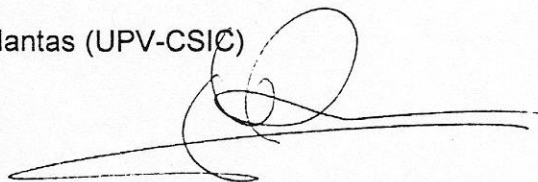
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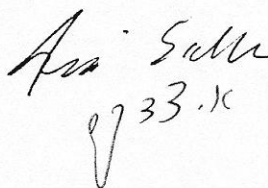
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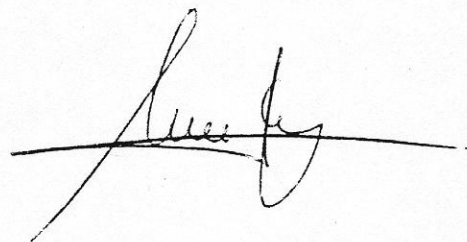
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